Amendments to the Claims:

Please amend Claims 2-13 and 18-19 as set forth below.

1. (Previously presented) A method for identifying an analyte nucleic acid in a sample comprising the steps of:

(a) providing a solid porous substrate, said substrate comprising a plurality of micro-channels, wherein said micro-channels have immobilized thereon a target molecule capable of binding to an analyte present in said sample; wherein said channels are further provided with

- analyte amplification components,
- a reporter system, and
- said sample;

(b) amplifying analyte nucleic acid molecules present within said sample; and

(c) allowing binding to take place between an amplified analyte nucleic acid obtained in step (b), said target molecule immobilized onto the channels of said substrate, and said reporter system, wherein said reporter system allows detecting whether binding has occurred between said target molecule and said analyte nucleic acid.

2. (Currently amended) The ~~A~~ method according to claim 1, wherein said reporter system is integrated within said target molecule.

3. (Currently amended) The ~~A~~ method according to claim 1 or 2, wherein said reporter system is capable of inducing a colour reaction and/or capable of bio-, chemi- or photoluminescence.

4. (Currently amended) The ~~A~~ method according to claim 3, wherein said reporter system is a fluorescence quenching system.

5. (Currently amended) The ~~A~~ method according to claim 4, wherein said fluorescence quenching system is a molecular beacon.

6. (Currently amended) The ~~A~~ method according to claim 1, wherein said detecting whether binding has occurred between said target molecule and said analyte nucleic acid in step (c) is carried out in real-time.

7. (Currently amended) The ~~A~~ method according to claim 1, wherein said amplification reaction is under isothermal conditions.

8. (Currently amended) The method according to claim 1, wherein said amplifying of said nucleic acid molecules in step (b) is by an amplification technique selected from the group comprising PCR, SDA, TYRAS, NASBA ,RCA, 3SR, and TMA.

9. (Currently amended) The ~~A~~ method according to claim 1, wherein said solid porous substrate is a flow-through substrate.

10. (Currently amended) The ~~A~~ method according to claim 1, wherein said solid porous substrate is a metallo oxide substrate.

11. (Currently amended) The ~~A~~ method according to claim 10, wherein said metallo-oxide substrate is an aluminum oxide substrate.

12. (Currently amended) The ~~A~~ method according to claim 1, wherein said substrate is incorporated in a housing.

13. (Currently amended) The ~~A~~ method according to claim 12, wherein said housing comprises a closing means, said closing means placed above the top surface of the substrate.

14. (Previously presented) The method of claim 1, which further comprises quantifying the analyte nucleic acid.

15. (Previously presented) The method of claim 1, which further comprises using the identified analyte nucleic acid for performing genotyping.

16. (Previously presented) The method of claim 1, which further comprises using the identified analyte nucleic acid for performing nucleic acid mutation detection.

17. (Previously presented) A device for identifying an analyte nucleic acid sequence in a sample comprising a porous substrate, said porous substrate comprising microchannels, said microchannels having immobilized thereon a target molecule and provided with amplification components for amplifying analyte nucleic acid molecules.

18. (Currently amended) The ~~A~~ device according to claim 17, wherein said microchannels having immobilized thereon a target molecule are additionally provided with a reporter system.

19. (Currently amended) The ~~A~~ device according to claim 18, wherein said reporter system is integrated within said immobilized target molecule.

20. (Original) A kit for identifying an analyte nucleic acid in a sample comprising nucleic acid molecules, said kit comprising a device according to any of claims 17 to 19.